```
    ATGTGGGTGACCAAACTCCTGCCAGCCCTGCTGCTGCAGCATGTCCTCCTGCATCTCCTC
  1 ---------+---------+---------+---------+---------+---------+  60
    TACACCCACTGGTTTGAGGACGGTCGGGACGACGACGTCGTACAGGAGGACGTAGAGGAG
  1 M  W  V  T  K  L  L  P  A  L  L  L  Q  H  V  L  L  H  L  L   20
    CTGCTCCCCATCGCCATCCCCTATGCAGAGGGACAAAGGAAAAGAAGAAATACAATTCAT
 61 ---------+---------+---------+---------+---------+---------+ 120
    GACGAGGGGTAGCGGTAGGGGATACGTCTCCCTGTTTCCTTTTCTTCTTTATGTTAAGTA
 21 L  L  P  I  A  I  P  Y  A  E  G  Q  R  K  R  R  N  T  I  H   40
    GAATTCAAAAAATCAGCAAAGACTACCCTAATCAAAATAGATCCAGCACTGAAGATAAAA
121 ---------+---------+---------+---------+---------+---------+ 180
    CTTAAGTTTTTTAGTCGTTTCTGATGGGATTAGTTTTATCTAGGTCGTGACTTCTATTTT
 41 E  F  K  K  S  A  K  T  T  L  I  K  I  D  P  A  L  K  I  K   60
    ACCAAAAAAGTGAATACTGCAGACCAATGTGCTAATAGATGTACTAGGAATAAAGGACTT
181 ---------+---------+---------+---------+---------+---------+ 240
    TGGTTTTTTCACTTATGACGTCTGGTTACACGATTATCTACATGATCCTTATTTCCTGAA
 61 T  K  K  V  N  T  A  D  Q  C  A  N  R  C  T  R  N  K  G  L   80
    CCATTCACTTGCAAGGCTTTTGTTTTTGATAAAGCAAGAAAACAATGCCTCTGGTTCCCC
241 ---------+---------+---------+---------+---------+---------+ 300
    GGTAAGTGAACGTTCCGAAAACAAAAACTATTTCGTTCTTTTGTTACGGAGACCAAGGGG
 81 P  F  T  C  K  A  F  V  F  D  K  A  R  K  Q  C  L  W  F  P   100
    TTCAATAGCATGTCAAGTGGAGTGAAAAAAGAATTTGGCCATGAATTTGACCTCTATGAA
301 ---------+---------+---------+---------+---------+---------+ 360
    AAGTTATCGTACAGTTCACCTCACTTTTTTCTTAAACCGGTACTTAAACTGGAGATACTT
101 F  N  S  M  S  S  G  V  K  K  E  F  G  H  E  F  D  L  Y  E   120
    AACAAAGACTACATTAGAAACTGCATCATTGGTAAAGGACGCAGCTACAAGGGAACAGTA
361 ---------+---------+---------+---------+---------+---------+ 420
    TTGTTTCTGATGTAATCTTTGACGTAGTAACCATTTCCTGCGTCGATGTTCCCTTGTCAT
121 N  K  D  Y  I  R  N  C  I  I  G  K  G  R  S  Y  K  G  T  V   140
    TCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAGTTCCATGATACCACACGAACAC
421 ---------+---------+---------+---------+---------+---------+ 480
    AGATAGTGATTCTCACCGTAGTTTACAGTCGGGACCTCAAGGTACTATGGTGTGCTTGTG
141 S  I  T  K  S  G  I  K  C  Q  P  W  S  S  M  I  P  H  E  H   160
```

FIG.1a-1

```
                AGCTATCGGGGTAAAGACCTACAGGAAAACTACTGTCGAAATCCTCGAGGGGAAGAAGGG
481             ---------+---------+---------+---------+---------+---------+ 540
                TCGATAGCCCCATTTCTGGATGTCCTTTTGATGACAGCTTTAGGAGCTCCCCTTCTTCCC
161             S  Y  R  G  K  D  L  Q  E  N  Y  C  R  N  P  R  G  E  E  G   180
                GGACCCTGGTGTTTCACAAGCAATCCAGAGGTACGCTACGAAGTCTGTGACATTCCTCAG
541             ---------+---------+---------+---------+---------+---------+ 600
                CCTGGGACCACAAAGTGTTCGTTAGGTCTCCATGCGATGCTTCAGACACTGTAAGGAGTC
181             G  P  W  C  F  T  S  N  P  E  V  R  Y  E  V  C  D  I  P  Q   200
                TGTTCAGAAGTTGAATGCATGACCTGCAATGGGGAGAGTTATCGAGGTCTCATGGATCAT
601             ---------+---------+---------+---------+---------+---------+ 660
                ACAAGTCTTCAACTTACGTACTGGACGTTACCCCTCTCAATAGCTCCAGAGTACCTAGTA
201             C  S  E  V  E  C  M  T  C  N  G  E  S  Y  R  G  L  M  D  H   220
                ACAGAATCAGGCAAGATTTGTCAGCGCTGGGATCATCAGACACCACACCGGCACAAATTC
661             ---------+---------+---------+---------+---------+---------+ 720
                TGTCTTAGTCCGTTCTAAACAGTCGCGACCCTAGTAGTCTGTGGTGTGGCCGTGTTTAAG
221             T  E  S  G  K  I  C  Q  R  W  D  H  Q  T  P  H  R  H  K  F   240
                TTGCCTGAAAGATATCCCGACAAGGGCTTTGATGATAATTATTGCCGCAATCCCGATGGC
721             ---------+---------+---------+---------+---------+---------+ 780
                AACGGACTTTCTATAGGGCTGTTCCCGAAACTACTATTAATAACGGCGTTAGGGCTACCG
241             L  P  E  R  Y  P  D  K  G  F  D  D  N  Y  C  R  N  P  D  G   260
                CAGCCGAGGCCATGGTGCTATACTCTTGACCCTCACACCCGCTGGGAGTACTGTGCAATT
781             ---------+---------+---------+---------+---------+---------+ 840
                GTCGGCTCCGGTACCACGATATGAGAACTGGGAGTGTGGGCGACCCTCATGACACGTTAA
261             Q  P  R  P  W  C  Y  T  L  D  P  H  T  R  W  E  Y  C  A  I   280
                AAAACATGCGCTGACAATACTATGAATGACACTGATGTTCCTTTGGAAACAACTGAATGC
841             ---------+---------+---------+---------+---------+---------+ 900
                TTTTGTACGCGACTGTTATGATACTTACTGTGACTACAAGGAAACCTTTGTTGACTTACG
281             K  T  C  A  D  N  T  M  N  D  T  D  V  P  L  E  T  T  E  C   300
                ATCCAAGGTCAAGGAGAAGGCTACAGGGGCACTGTCAATACCATTTGGAATGGAATTCCA
901             ---------+---------+---------+---------+---------+---------+ 960
                TAGGTTCCAGTTCCTCTTCCGATGTCCCCGTGACAGTTATGGTAAACCTTACCTTAAGGT
301             I  Q  G  Q  G  E  G  Y  R  G  T  V  N  T  I  W  N  G  I  P   320
                TGTCAGCGTTGGGATTCTCAGTATCCTCACGAGCATGACATGACTCCTGAAAATTTCAAG
961             ---------+---------+---------+---------+---------+---------+ 1020
                ACAGTCGCAACCCTAAGAGTCATAGGAGTGCTCGTACTGTACTGAGGACTTTTAAAGTTC
321             C  Q  R  W  D  S  Q  Y  P  H  E  H  D  M  T  P  E  N  F  K   340
                TGCAAGGACCTACGAGAAAATTACTGCCGAAATCCAGATGGGTCTGAATCACCCTGGTGT
1021            ---------+---------+---------+---------+---------+---------+ 1080
                ACGTTCCTGGATGCTCTTTTAATGACGGCTTTAGGTCTACCCAGACTTAGTGGGACCACA
341             C  K  D  L  R  E  N  Y  C  R  N  P  D  G  S  E  S  P  W  C   360
                TTTACCACTGATCCAAACATCCGAGTTGGCTACTGCTCCCAAATTCCAAACTGTGATATG
1081            ---------+---------+---------+---------+---------+---------+ 1140
                AAATGGTGACTAGGTTTGTAGGCTCAACCGATGACGAGGGTTTAAGGTTTGACACTATAC
361             F  T  T  D  P  N  I  R  V  G  Y  C  G  Q  I  P  N  C  D  M   380
```

FIG.1a-2

```
                TCACATGGACAAGATTGTTATCGTGGGAATGGCAAAAATTATATGGGCAACTTATCCCAA
1141            ---------+---------+---------+---------+---------+---------+ 1200
                AGTGTACCTGTTCTAACAATAGCACCCTTACCGTTTTTAATATACCCGTTGAATAGGGTT
 381            S  H  G  Q  D  C  Y  R  G  N  G  K  N  Y  M  G  N  L  S  Q    400
                ACAAGATCTGGACTAACATGTTCAATGTGGGACAAGAACATGGAAGACTTACATCGTCAT
1201            ---------+---------+---------+---------+---------+---------+ 1260
                TGTTCTAGACCTGATTGTACAAGTTACACCCTGTTCTTGTACCTTCTGAATGTAGCAGTA
 401            T  R  S  G  L  T  C  S  M  W  D  K  N  M  E  D  L  H  R  H    420
                ATCTTCTGGGAACCAGATGCAAGTAAGCTGAATGAGAATTACTGCCGAAATCCAGATGAT
1261            ---------+---------+---------+---------+---------+---------+ 1320
                TAGAAGACCCTTGGTCTACGTTCATTCGACTTACTCTTAATGACGGCTTTAGGTCTACTA
 421            I  F  W  E  P  D  A  S  K  L  N  E  N  Y  C  R  N  P  D  D    440
                GACGCTCATGGACCCTGGTGCTACACGGGAAATCCACTCATTCCTTGGGATTATTGCCCT
1321            ---------+---------+---------+---------+---------+---------+ 1380
                CTGCGAGTACCTGGGACCACGATGTGCCCTTTAGGTGAGTAAGGAACCCTAATAACGGGA
 441            D  A  H  G  P  W  C  Y  T  G  N  P  L  I  P  W  D  Y  C  P    460
                ATTTCTCGTTGTGAAGGTGATACCACACCTACAATAGTCAATTTAGACCATCCCGTAATA
1381            ---------+---------+---------+---------+---------+---------+ 1440
                TAAAGAGCAACACTTCCACTATGGTGTGGATGTTATCAGTTAAATCTGGTAGGGCATTAT
 461            I  S  R  C  E  G  D  T  T  P  T  I  V  N  L  D  H  P  V  I    480
                TCTTGTGCCAAAACGAAACAATTGCGAGTTGTAAATGGGATTCCAACACGAACAAACATA
1441            ---------+---------+---------+---------+---------+---------+ 1500
                AGAACACGGTTTTGCTTTGTTAACGCTCAACATTTACCCTAAGGTTGTGCTTGTTTGTAT
 481            S  C  A  K  T  K  Q  L  R  V  V  N  G  I  P  T  R  T  N  I    500
                GGATGGATGGTTAGTTTGAGATACAGAAATAAACATATCTGCGGAGGATCATTGATAAAG
1501            ---------+---------+---------+---------+---------+---------+ 1560
                CCTACCTACCAATCAAACTCTATGTCTTTATTTGTATAGACGCCTCCTAGTAACTATTTC
 501            G  W  M  V  S  L  R  Y  R  N  K  H  I  C  G  G  S  L  I  K    520
                GAGAGTTGGGTTCTTACTGCACGACAGTGTTTCCCTTCTCGAGACTTGAAAGATTATGAA
1561            ---------+---------+---------+---------+---------+---------+ 1620
                CTCTCAACCCAAGAATGACGTGCTGTCACAAAGGGAAGAGCTCTGAACTTTCTAATACTT
 521            E  S  W  V  L  T  A  R  Q  C  F  P  S  R  D  L  K  D  Y  E    540
                GCTTGGCTTGGAATTCATGATGTCCACGGAAGAGGAGATGAGAAATGCAAACAGGTTCTC
1621            ---------+---------+---------+---------+---------+---------+ 1680
                CGAACCGAACCTTAAGTACTACAGGTGCCTTCTCCTCTACTCTTTACGTTTGTCCAAGAG
 541            A  W  L  G  I  H  D  V  H  G  R  G  D  E  K  C  K  Q  V  L    560
                AATGTTTCCCAGCTGGTATATGGCCCTGAAGGATCAGATCTGGTTTTAATGAAGCTTGCC
1681            ---------+---------+---------+---------+---------+---------+ 1740
                TTACAAAGGGTCGACCATATACCGGGACTTCCTAGTCTAGACCAAAATTACTTCGAACGG
 561            N  V  S  Q  L  V  Y  G  P  E  G  S  D  L  V  L  M  K  L  A    580
                AGGCCTGCTGTCCTGGATGATTTTGTTAGTACGATTGATTTACCTAATTATGGATGCACA
1741            ---------+---------+---------+---------+---------+---------+ 1800
                TCCGGACGACAGGACCTACTAAAACAATCATGCTAACTAAATGGATTAATACCTACGTGT
 581            R  P  A  V  L  D  D  F  V  S  T  I  D  L  P  N  Y  G  C  T    600
```

FIG.1a-3

```
                ATTCCTGAAAAGACCAGTTGCAGTGTTTATGGCTGGGGCTACACTGGATTGATCAACTAT
1801            ---------+---------+---------+---------+---------+---------+ 1860
                TAAGGACTTTTCTGGTCAACGTCACAAATACCGACCCCGATGTGACCTAACTAGTTGATA
 601            I  P  E  K  T  S  C  S  V  Y  G  W  G  Y  T  G  L  I  N  Y    620
                GATGGCCTATTACGAGTGGCACATCTCTATATAATGGGAAATGAGAAATGCAGCCAGCAT
1861            ---------+---------+---------+---------+---------+---------+ 1920
                CTACCGGATAATGCTCACCGTGTAGAGATATATTACCCTTTACTCTTTACGTCGGTCGTA
 621            D  G  L  L  R  V  A  H  L  Y  I  M  G  N  E  K  C  S  Q  H    640
                CATCGAGGGAAGGTGACTCTGAATGAGTCTGAAATATGTGCTGGGGCTGAAAAGATTGGA
1921            ---------+---------+---------+---------+---------+---------+ 1980
                GTAGCTCCCTTCCACTGAGACTTACTCAGACTTTATACACGACCCCGACTTTTCTAACCT
 641            H  R  G  K  V  T  L  N  E  S  E  I  C  A  G  A  E  K  I  G    660
                TCAGGACCATGTGAGGGGGATTATGGTGGCCCACTTGTTTGTGAGCAACATAAAATGAGA
1981            ---------+---------+---------+---------+---------+---------+ 2040
                AGTCCTGGTACACTCCCCCTAATACCACCGGGTGAACAAACACTCGTTGTATTTTACTCT
 661            S  G  P  C  E  G  D  Y  G  G  P  L  V  C  E  Q  H  K  M  R    680
                ATGGTTCTTGGTGTCATTGTTCCTGGTCGTGGATGTGCCATTCCAAATCGTCCTGGTATT
2041            ---------+---------+---------+---------+---------+---------+ 2100
                TACCAAGAACCACAGTAACAAGGACCAGCACCTACACGGTAAGGTTTAGCAGGACCATAA
 681            M  V  L  G  V  I  V  P  G  R  G  C  A  I  P  N  R  P  G  I    700
                TTTGTCCGAGTAGCATATTATGCAAAATGGATACACAAAATTATTTTAACATATAAGGTA
2101            ---------+---------+---------+---------+---------+---------+ 2160
                AAACAGGCTCATCGTATAATACGTTTTACCTATGTGTTTTAATAAAATTGTATATTCCAT
 701            F  V  R  V  A  Y  Y  A  K  W  I  H  K  I  I  L  T  Y  K  V    720
                CCACAGTCATAG
2161            ---------+--  2172
                GGTGTCAGTATC
 721            P  Q  S  *     723
```

FIG.1a-4

```
    ATGGGGTGGCTCCCACTCCTGCTGCTTCTGACTCAATGCTTAGGGGTCCCTGGGCAGCGC
  1 ---------+---------+---------+---------+---------+---------+  60
    TACCCCACCGAGGGTGAGGACGACGAAGACTGAGTTACGAATCCCCAGGGACCCGTCGCG
  1 M  G  W  L  P  L  L  L  L  L  T  Q  C  L  G  V  P  G  Q  R   20
    TCGCCATTGAATGACTTCCAAGTGCTCCGGGGCACRGAGCTACAGCACCTGCTACATGCG
 61 ---------+---------+---------+---------+---------+---------+ 120
    AGCGGTAACTTACTGAAGGTTCACGAGGCCCCGTGTCTCGATGTCGTGGACGATGTACGC
 21 S  P  L  N  D  F  Q  V  L  R  G  T  E  L  Q  H  L  L  H  A   40
    GTGGTGCCCGGGCCTTGGCAGGAGGATGTGGCAGATGCTGAAGAGTGTGCTGGTCGCTGT
121 ---------+---------+---------+---------+---------+---------+ 180
    CACCACGGGCCCGGAACCGTCCTCCTACACCGTCTACGACTTCTCACACGACCAGCGACA
 41 V  V  P  G  P  W  Q  E  D  V  A  D  A  E  E  C  A  G  R  C   60
    GGGCCCTTAATGGACTGCCGGGCCTTCCACTACAACGTGAGCAGCCATGGTTGCCAACTG
181 ---------+---------+---------+---------+---------+---------+ 240
    CCCGGGAATTACCTGACGGCCCGGAAGGTGATGTTGCACTCGTCGGTACCAACGGTTGAC
 61 G  P  L  M  D  C  R  A  F  H  Y  N  V  S  S  H  G  C  Q  L   80
    CTGCCATGGACTCAACACTCGCCCCACACGAGGCTGCGGCGTTCTGGGCGCTGTGACCTC
241 ---------+---------+---------+---------+---------+---------+ 300
    GACGGTACCTGAGTTGTGAGCGGGGTGTGCTCCGACGCCGCAAGACCCGCGACACTGGAG
 81 L  P  W  T  Q  H  S  P  H  T  R  L  R  R  S  G  R  C  D  L   100
    TTCCAGAAGAAAGACTACGTACGGACCTGCATCATGAACAATGGGGTTGGGTACCGGGGC
301 ---------+---------+---------+---------+---------+---------+ 360
    AAGGTCTTCTTTCTGATGCATGCCTGGACGTAGTACTTGTTACCCCAACCCATGGCCCCG
101 F  Q  K  K  D  Y  V  R  T  C  I  M  N  N  G  V  G  Y  R  G   120
    ACCATGGCCACGACCGTGGGTGGCCTGCCCTGCCAGGCTTGGAGCCACAAGTTCCCGAAT
361 ---------+---------+---------+---------+---------+---------+ 420
    TGGTACCGGTGCTGGCACCCACCGGACGGGACGGTCCGAACCTCGGTGTTCAAGGGCTTA
121 T  M  A  T  T  V  G  G  L  P  C  Q  A  W  S  H  K  F  P  N   140
    GATCACAAGTACACGCCCACTCTCCGGAATGGCCTGGAAGAGAACTTCTGCCGTAACCCT
421 ---------+---------+---------+---------+---------+---------+ 480
    CTAGTGTTCATGTGCGGGTGAGAGGCCTTACCGGACCTTCTCTTGAAGACGGCATTGGGA
141 D  H  K  Y  T  P  T  L  R  N  G  L  E  E  N  F  C  R  N  P   160
```

FIG.1b-1

```
                GATGGCGACCCCGGAGGTCCTTGGTGCTACACAACAGACCCTGCTGTGCGCTTCCAGAGC
481             ---------+---------+---------+---------+---------+---------+ 540
                CTACCGCTGGGGCCTCCAGGAACCACGATGTGTTGTCTGGGACGACACGCGAAGGTCTCG
161             D  G  D  P  G  G  P  W  C  Y  T  T  D  P  A  V  R  F  Q  S    180
                TGCGGCATCAAATCCTGCCGGGAGGCCGCGTGTGTCTGGTGCAATGGCGAGGAATACCGC
531             ---------+---------+---------+---------+---------+---------+ 600
                ACGCCGTAGTTTAGGACGGCCCTCCGGCGCACACAGACCACGTTACCGCTCCTTATGGCG
181             C  G  I  K  S  C  R  E  A  A  C  V  W  C  N  G  E  E  Y  R    200
                GGCGCGGTAGACCGCACGGAGTCAGGGCGCGAGTGCCAGCGCTGGGATCTTCAGCACCCG
601             ---------+---------+---------+---------+---------+---------+ 660
                CCGCGCCATCTGGCGTGCCTCAGTCCCGCGCTCACGGTCGCGACCCTAGAAGTCGTGGGC
201             G  A  V  D  R  T  E  S  G  R  E  C  Q  R  W  D  L  Q  H  P    220
                CACCAGCACCCCTTCGAGCCGGGCAAGTTCCTCGACCAAGGTCTGGACGACAACTATTGC
661             ---------+---------+---------+---------+---------+---------+ 720
                GTGGTCGTGGGGAAGCTCGGCCCGTTCAAGGAGCTGGTTCCAGACCTGCTGTTGATAACG
221             H  Q  H  P  F  E  P  G  K  F  L  D  Q  G  L  D  D  N  Y  C    240
                CGGAATCCTGACGGCTCCGAGCGGCCATGGTGCTACACTACGGATCCGCAGATCGAGCGA
721             ---------+---------+---------+---------+---------+---------+ 780
                GCCTTAGGACTGCCGAGGCTCGCCGGTACCACGATGTGATGCCTAGGCGTCTAGCTCGCT
241             R  N  P  D  G  S  E  R  P  W  C  Y  T  T  D  P  Q  I  E  R    260
                GAGTTCTGTGACCTCCCCCGCTGCGGGTCCGAGGCACAGCCCCGCCAAGAGGCCACAACT
781             ---------+---------+---------+---------+---------+---------+ 840
                CTCAAGACACTGGAGGGGGCGACGCCCAGGCTCCGTGTCGGGGCGGTTCTCCGGTGTTGA
261             E  F  C  D  L  P  R  C  G  S  E  A  Q  P  R  Q  E  A  T  T    280
                GTCAGCTGCTTCCGCGGGAAGGGTGAGGGCTACCGGGGCACAGCCAATACCACCACTGCG
841             ---------+---------+---------+---------+---------+---------+ 900
                CAGTCGACGAAGGCGCCCTTCCCACTCCCGATGGCCCCGTGTCGGTTATGGTGGTGACGC
281             V  S  C  F  R  G  K  G  E  G  Y  R  G  T  A  N  T  T  T  A    300
                GGCGTACCTTGCCAGCGTTGGGACGCGCAAATCCCGCATCAGCACCGATTTACGCCAGAA
901             ---------+---------+---------+---------+---------+---------+ 960
                CCGCATGGAACGGTCGCAACCCTGCGCGTTTAGGGCGTAGTCGTGGCTAAATGCGGTCTT
301             G  V  P  C  Q  R  W  D  A  Q  I  P  H  Q  H  R  F  T  P  E    320
                AAATACGCGTGCAAAGACCTTCGGGAGAACTTCTGCCGGAACCCCGACGGCTCAGAGGCG
961             ---------+---------+---------+---------+---------+---------+ 1020
                TTTATGCGCACGTTTCTGGAAGCCCTCTTGAAGACGGCCTTGGGGCTGCCGAGTCTCCGC
321             K  Y  A  C  K  D  L  R  E  N  F  C  R  N  P  D  G  S  E  A    340
                CCCTGGTGCTTCACACTGCGGCCCGGCATGCGCGCGGCCTTTTGCTACCAGATCCGGCGT
1021            ---------+---------+---------+---------+---------+---------+ 1080
                GGGACCACGAAGTGTGACGCCGGGCCGTACGCGCGCCGGAAAACGATGGTCTAGGCCGCA
341             P  W  C  F  T  L  R  P  G  M  R  A  A  F  C  Y  Q  I  R  R    360
                TGTACAGACGACGTGCGGCCCCAGGACTGCTACCACGGCGCAGGGGAGCAGTACCGCGGC
1081            ---------+---------+---------+---------+---------+---------+ 1140
                ACATGTCTGCTGCACGCCGGGGTCCTGACGATGGTGCCGCGTCCCCTCGTCATGGCGCCG
361             C  T  D  D  V  R  P  Q  D  C  Y  H  G  A  G  E  Q  Y  R  G    380
```

FIG.1b-2

```
                ACGGTCAGCAAGACCCGCAAGGGTGTCCAGTGCCAGCGCTGGTCCGCTGAGACGCCGCAC
1141            ---------+---------+---------+---------+---------+---------+ 1200
                TGCCAGTCGTTCTGGGCGTTCCCACAGGTCACGGTCGCGACCAGGCGACTCTGCGGCGTG
 381            T  V  S  K  T  R  K  G  V  Q  C  Q  R  W  S  A  E  T  P  H    400
                AAGCCGCAGTTCACGTTTACCTCCGAACCGCATGCACAACTGGAGGAGAACTTCTGCCGG
1201            ---------+---------+---------+---------+---------+---------+ 1260
                TTCGGCGTCAAGTGCAAATGGAGGCTTGGCGTACGTGTTGACCTCCTCTTGAAGACGGCC
 401            K  P  Q  F  T  F  T  S  E  P  H  A  Q  L  E  E  N  F  C  R    420
                AACCCAGATGGGGATAGCCATGGGCCCTGGTGCTACACGATGGACCCAAGGACCCCATTC
1261            ---------+---------+---------+---------+---------+---------+ 1320
                TTGGGTCTACCCCTATCGGTACCCGGGACCACGATGTGCTACCTGGGTTCCTGGGGTAAG
 421            N  P  D  G  D  S  H  G  P  W  C  Y  T  M  D  P  R  T  P  F    440
                GACTACTGTGCCCTGCGACGCTGCGCTGATGACCAGCCGCCATCAATCCTGGACCCCCCA
1321            ---------+---------+---------+---------+---------+---------+ 1380
                CTGATGACACGGGACGCTGCGACGCGACTACTGGTCGGCGGTAGTTAGGACCTGGGGGGT
 441            D  Y  C  A  L  R  R  C  A  D  D  Q  P  P  S  I  L  D  P  P    460
                GACCAGGTGCAGTTTGAGAAGTGTGGCAAGAGGGTGGATCGGCTGGATCAGCGGCGTTCC
1381            ---------+---------+---------+---------+---------+---------+ 1440
                CTGGTCCACGTCAAACTCTTCACACCGTTCTCCCACCTAGCCGACCTAGTCGCCGCAAGG
 461            D  Q  V  Q  F  E  K  C  G  K  R  V  D  R  L  D  Q  R  R  S    480
                AAGCTGCGCGTGGTTGGGGGCCATCCGGGCAACTCACCCTGGACAGTCAGCTTGCGGAAT
1441            ---------+---------+---------+---------+---------+---------+ 1500
                TTCGACGCGCACCAACCCCCGGTAGGCCCGTTGAGTGGGACCTGTCAGTCGAACGCCTTA
 481            K  L  R  V  V  G  G  H  P  G  N  S  P  W  T  V  S  L  R  N    500
                CGGCAGGGCCAGCATTTCTGCGGGGGGTCTCTAGTGAAGGAGCAGTGGATACTGACTGCC
1501            ---------+---------+---------+---------+---------+---------+ 1560
                GCCGTCCCGGTCGTAAAGACGCCCCCCAGAGATCACTTCCTCGTCACCTATGACTGACGG
 501            R  Q  G  Q  H  F  C  G  G  S  L  V  K  E  Q  W  I  L  T  A    520
                CGGCAGTGCTTCTCCTCCTGCCATATGCCTCTCACGGGCTATGAGGTATGGTTGGGCACC
1561            ---------+---------+---------+---------+---------+---------+ 1620
                GCCGTCACGAAGAGGAGGACGGTATACGGAGAGTGCCCGATACTCCATACCAACCCGTGG
 521            R  Q  C  F  S  S  C  H  M  P  L  T  G  Y  E  V  W  L  G  T    540
                CTGTTCCAGAACCCACAGCATGGAGAGCCAAGCCTACAGCGGGTCCCAGTAGCCAAGATG
1621            ---------+---------+---------+---------+---------+---------+ 1680
                GACAAGGTCTTGGGTGTCGTACCTCTCGGTTCGGATGTCGCCCAGGGTCATCGGTTCTAC
 541            L  F  Q  N  P  Q  H  G  E  P  S  L  Q  R  V  P  V  A  K  M    560
                GTGTGTGGGCCCTCAGGCTCCCAGCTTGTCCTGCTCAAGCTGGAGAGATCTGTGACCCTG
1681            ---------+---------+---------+---------+---------+---------+ 1740
                CACACACCCGGGAGTCCGAGGGTCGAACAGGACGAGTTCGACCTCTCTAGACACTGGGAC
 561            V  C  G  P  S  G  S  Q  L  V  L  L  K  L  E  R  S  V  T  L    580
                AACCAGCGTGTGGCCCTGATCTGCCTGCCCCCTGAATGGTATGTGGTGCCTCCAGGGACC
1741            ---------+---------+---------+---------+---------+---------+ 1800
                TTGGTCGCACACCGGGACTAGACGGACGGGGGACTTACCATACACCACGGAGGTCCCTGG
 581            N  Q  R  V  A  L  I  C  L  P  P  E  W  Y  V  V  P  P  G  T    600
```

FIG.1b-3

```
      AAGTGTGAGATTGCAGGCTGGGGTGAGACCAAAGGTACGGGTAATGACACAGTCCTAAAT
1801  ---------+---------+---------+---------+---------+---------+  1860
      TTCACACTCTAACGTCCGACCCCACTCTGGTTTCCATGCCCATTACTGTGTCAGGATTTA
 601  K  C  E  I  A  G  W  G  E  T  K  G  T  G  N  D  T  V  L  N    620
      GTGGCCTTTCTGAATGTTATCTCCAACCAGGAGTGTAACATCAAGCACCGAGGACGTGTG
1861  ---------+---------+---------+---------+---------+---------+  1920
      CACCGGAAAGACTTACAATAGAGGTTGGTCCTCACATTGTAGTTCGTGGCTCCTGCACAC
 621  V  A  F  L  N  V  I  S  N  Q  E  C  N  I  K  H  R  G  R  V    640
      CGGGAGAGTGAGATGTGCACTGAGGGACTGTTGGCCCCTGTGGGGGCCTGTGAGGGTGAC
1921  ---------+---------+---------+---------+---------+---------+  1980
      GCCCTCTCACTCTACACGTGACTCCCTGACAACCGGGGACACCCCCGGACACTCCCACTG
 641  R  E  S  E  M  C  T  E  G  L  L  A  P  V  G  A  C  E  G  D    660
      TACGGGGGCCCACTTGCCTGCTTTACCCACAACTGCTGGGTCCTGGAAGGAATTATAATC
1981  ---------+---------+---------+---------+---------+---------+  2040
      ATGCCCCCGGGTGAACGGACGAAATGGGTGTTGACGACCCAGGACCTTCCTTAATATTAG
 661  Y  G  G  P  L  A  C  F  T  H  N  C  W  V  L  E  G  I  I  I    680
      CCCAACCGAGTATGCGCAAGGTCCCGCTGGCCAGCTGTCTTCACGCGTGTCTCTGTGTTT
2041  ---------+---------+---------+---------+---------+---------+  2100
      GGGTTGGCTCATACGCGTTCCAGGGCGACCGGTCGACAGAAGTGCGCACAGAGACACAAA
 681  P  N  R  V  C  A  R  S  R  W  P  A  V  F  T  R  V  S  V  F    700
      GTGGACTGGATTCACAAGGTCATGAGACTGGGTTAG
2101  ---------+---------+---------+------  2136
      CACCTGACCTAAGTGTTCCAGTACTCTGACCCAATC
 701  V  D  W  I  H  K  V  M  R  L  G  *     711
```

FIG.1b-4

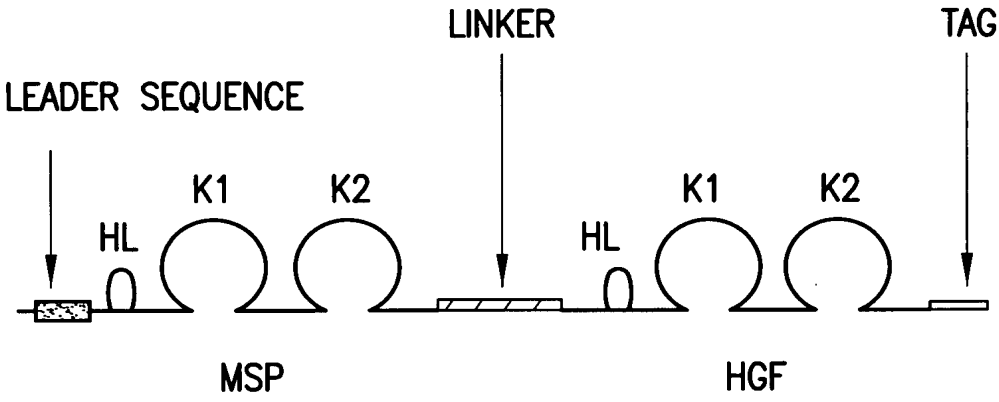

FIG.2a

```
                GAATTCCACCATGGGGTGGCTCCCACTCCTGCTGCTTCTGACTCAATGCTTAGGGGTCCC
1               ---------+---------+---------+---------+---------+---------+ 60
                CTTAAGGTGGTACCCCACCGAGGGTGAGGACGACGAAGACTGAGTTACGAATCCCCAGGG
1                       M  G  W  L  P  L  L  L  L  L  T  Q  C  L  G  V  P   17
                TGGGCAGCGCTCGCCATTGAATGACTTCCAAGTGCTCCGGGGCACAGAGCTACAGCACCT
61              ---------+---------+---------+---------+---------+---------+ 120
                ACCCGTCGCGAGCGGTAACTTACTGAAGGTTCACGAGGCCCCGTGTCTCGATGTCGTGGA
18               G  Q  R  S  P  L  N  D  F  Q  V  L  R  G  T  E  L  Q  H  L   37
                GCTACATGCGGTGGTGCCCGGGCCTTGGCAGGAGGATGTGGCAGATGCTGAAGAGTGTGC
121             ---------+---------+---------+---------+---------+---------+ 180
                CGATGTACGCCACCACGGGCCCGGAACCGTCCTCCTACACCGTCTACGACTTCTCACACG
38               L  H  A  V  V  P  G  P  W  Q  E  D  V  A  D  A  E  E  C  A   57
                TGGTCGCTGTGGGCCCTTAATGGACTGCCGGGCCTTCCACTACAACGTGAGCAGCCATGG
181             ---------+---------+---------+---------+---------+---------+ 240
                ACCAGCGACACCCGGGAATTACCTGACGGCCCGGAAGGTGATGTTGCACTCGTCGGTACC
58               G  R  C  G  P  L  M  D  C  R  A  F  H  Y  N  V  S  S  H  G   77
                TTGCCAACTGCTGCCATGGACTCAACACTCGCCCCACACGAGGCTGCGGCGTTCTGGGCG
241             ---------+---------+---------+---------+---------+---------+ 300
                AACGGTTGACGACGGTACCTGAGTTGTGAGCGGGGTGTGCTCCGACGCCGCAAGACCCGC
78               C  Q  L  L  P  W  T  Q  H  S  P  H  T  R  L  R  R  S  G  R   97
                CTGTGACCTCTTCCAGAAGAAAGACTACGTACGGACCTGCATCATGAACAATGGGGTTGG
301             ---------+---------+---------+---------+---------+---------+ 360
                GACACTGGAGAAGGTCTTCTTTCTGATGCATGCCTGGACGTAGTACTTGTTACCCCAACC
98               C  D  L  F  Q  K  K  D  Y  V  R  T  C  I  M  N  N  G  V  G   117
                GTACCGGGGCACCATGGCCACGACCGTGGGTGGCCTGCCCTGCCAGGCTTGGAGCCACAA
361             ---------+---------+---------+---------+---------+---------+ 420
                CATGGCCCCGTGGTACCGGTGCTGGCACCCACCGGACGGGACGGTCCGAACCTCGGTGTT
118              Y  R  G  T  M  A  T  T  V  G  G  L  P  C  Q  A  W  S  H  K   137
                GTTCCCGAATGATCACAAGTACACGCCCACTCTCCGGAATGGCCTGGAAGAGAACTTCTG
421             ---------+---------+---------+---------+---------+---------+ 480
                CAAGGGCTTACTAGTGTTCATGTGCGGGTGAGAGGCCTTACCGGACCTTCTCTTGAAGAC
138              F  P  N  D  H  K  Y  T  P  T  L  R  N  G  L  E  E  N  F  C   157
                CCGTAACCCTGATGGCGACCCCGGAGGTCCTTGGTGCTACACAACAGACCCTGCTGTGCG
481             ---------+---------+---------+---------+---------+---------+ 540
                GGCATTGGGACTACCGCTGGGGCCTCCAGGAACCACGATGTGTTGTCTGGGACGACACGC
159              R  N  P  D  G  D  P  G  G  P  W  C  Y  T  T  D  P  A  V  R   177
```

FIG.2b-1

```
                CTTCCAGAGCTGCGGCATCAAATCCTGCCGGGAGGCCGCGTGTGTCTGGTGCAATGGCGA
541 ---------+---------+---------+---------+---------+---------+---------+ 600
                GAAGGTCTCGACGCCGTAGTTTAGGACGGCCCTCCGGCGCACACAGACCACGTTACCGCT
178   F  Q  S  C  G  I  K  S  C  R  E  A  A  C  V  W  C  N  G  E           197
                GGAATACCGCGGCGCGGTAGACCGCACGGAGTCAGGGCGCGAGTGCCAGCGCTGGGATCT
601 ---------+---------+---------+---------+---------+---------+---------+ 660
                CCTTATGGCGCCGCGCCATCTGGCGTGCCTCAGTCCCGCGCTCACGGTCGCGACCCTAGA
198   E  Y  R  G  A  V  D  R  T  E  S  G  R  E  C  Q  R  W  D  L           217
                TCAGCACCCGCACCAGCACCCCTTCGAGCCGGGCAAGTTCCTCGACCAAGGTCTGGACGA
661 ---------+---------+---------+---------+---------+---------+---------+ 720
                AGTCGTGGGCGTGGTCGTGGGGAAGCTCGGCCCGTTCAAGGAGCTGGTTCCAGACCTGCT
218   Q  H  P  H  Q  H  P  F  E  P  G  K  F  L  D  Q  G  L  D  D           237
                CAACTATTGCCGGAATCCTGACGGCTCCGAGCGGCCATGGTGCTACACTACGGATCCGCA
721 ---------+---------+---------+---------+---------+---------+---------+ 780
                GTTGATAACGGCCTTAGGACTGCCGAGGCTCGCCGGTACCACGATGTGATGCCTAGGCGT
238   N  Y  C  R  N  P  D  G  S  E  R  P  W  C  Y  T  T  D  P  Q           257
                GATCGAGCGAGAGTTCTGTGACCTCCCCCGCTGCGGGTCCGAGGCACAGCCCCGCCTCGA
781 ---------+---------+---------+---------+---------+---------+---------+ 840
                CTAGCTCGCTCTCAAGACACTGGAGGGGGCGACGCCCAGGCTCCGTGTCGGGGCGGAGCT
258   I  E  R  E  F  C  D  L  P  R  C  G  S  E  A  Q  P  R  L  E           277
                GGGCGGTGGCGGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTCTAGAGGGACAAAG
841 ---------+---------+---------+---------+---------+---------+---------+ 900
                CCCGCCACCGCCAAGACCACCGCCACCGAGGCCGCCACCGCCAAGAGATCTCCCTGTTTC
278   G  G  G  G  S  G  G  G  G  S  G  G  G  G  S  L  E  G  Q  R           297
                GAAAAGAAGAAATACAATTCATGAATTCAAAAAATCAGCAAAGACTACCCTAATCAAAAT
901 ---------+---------+---------+---------+---------+---------+---------+ 960
                CTTTTCTTCTTTATGTTAAGTACTTAAGTTTTTTAGTCGTTTCTGATGGGATTAGTTTTA
298   K  R  R  N  T  I  H  E  F  K  K  S  A  K  T  T  L  I  K  I           317
                AGATCCAGCACTGAAGATAAAAACCAAAAAAGTGAATACTGCAGACCAATGTGCTAATAG
961 ---------+---------+---------+---------+---------+---------+---------+ 1020
                TCTAGGTCGTGACTTCTATTTTTGGTTTTTTCACTTATGACGTCTGGTTACACGATTATC
318   D  P  A  L  K  I  K  T  K  K  V  N  T  A  D  Q  C  A  N  R           337
                ATGTACTAGGAATAAAGGACTTCCATTCACTTGCAAGGCTTTTGTTTTTGATAAAGCAAG
1021 ---------+---------+---------+---------+---------+---------+---------+ 1080
                TACATGATCCTTATTTCCTGAAGGTAAGTGAACGTTCCGAAAACAAAAACTATTTCGTTC
338   C  T  R  N  K  G  L  P  F  T  C  K  A  F  V  F  D  K  A  R           357
                AAAACAATGCCTCTGGTTCCCCTTCAATAGCATGTCAAGTGGAGTGAAAAAAGAATTTGG
1081 ---------+---------+---------+---------+---------+---------+---------+ 1140
                TTTTGTTACGGAGACCAAGGGGAAGTTATCGTACAGTTCACCTCACTTTTTTCTTAAACC
358   K  Q  C  L  W  F  P  F  N  S  M  S  S  G  V  K  K  E  F  G           377
                CCATGAATTTGACCTCTATGAAAACAAAGACTACATTAGAAACTGCATCATTGGTAAAGG
1141 ---------+---------+---------+---------+---------+---------+---------+ 1200
                GGTACTTAAACTGGAGATACTTTTGTTTCTGATGTAATCTTTGACGTAGTAACCATTTCC
378   H  E  F  D  L  Y  E  N  H  D  Y  I  R  N  C  I  I  G  K  G           397
```

FIG.2b-2

```
      ACGCAGCTACAAGGGAACAGTATCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAG
1201  ---------+---------+---------+---------+---------+---------+ 1260
      TGCGTCGATGTTCCCTTGTCATAGATAGTGATTCTCACCGTAGTTTACAGTCGGGACCTC
 398   R  S  Y  K  G  T  V  S  I  T  K  S  G  I  K  C  Q  P  W  S   417
      TTCCATGATACCACACGAACACAGCTATCGGGGTAAAGACCTACAGGAAAACTACTGTCG
1261  ---------+---------+---------+---------+---------+---------+ 1320
      AAGGTACTATGGTGTGCTTGTGTCGATAGCCCCATTTCTGGATGTCCTTTTGATGACAGC
 418   S  M  I  P  H  E  H  S  Y  R  G  K  D  L  Q  E  N  Y  C  R   437
      AAATCCTCGAGGGGAAGAAGGGGGACCCTGGTGTTTCACAAGCAATCCAGAGGTACGCTA
1321  ---------+---------+---------+---------+---------+---------+ 1380
      TTTAGGAGCTCCCCTTCTTCCCCCTGGGACCACAAAGTGTTCGTTAGGTCTCCATGCGAT
 438   N  P  R  G  E  E  G  G  P  W  C  F  T  S  N  P  E  V  R  Y   457
      CGAAGTCTGTGACATTCCTCAGTGTTCAGAAGTTGAATGCATGACCTGCAATGGGGAGAG
1381  ---------+---------+---------+---------+---------+---------+ 1440
      GCTTCAGACACTGTAAGGAGTCACAAGTCTTCAACTTACGTACTGGACGTTACCCCTCTC
 458   E  V  C  D  I  P  Q  C  S  E  V  E  C  M  T  C  N  G  E  S   477
      TTATCGAGGTCTCATGGATCATACAGAATCAGGCAAGATTTGTCAGCGCTGGGATCATCA
1441  ---------+---------+---------+---------+---------+---------+ 1500
      AATAGCTCCAGAGTACCTAGTATGTCTTAGTCCGTTCTAAACAGTCGCGACCCTAGTAGT
 478   Y  R  G  L  M  D  H  T  E  S  G  K  I  C  Q  R  W  D  H  Q   497
      GACACCACACCGGCACAAATTCTTGCCTGAAAGATATCCCGACAAGGGCTTTGATGATAA
1501  ---------+---------+---------+---------+---------+---------+ 1560
      CTGTGGTGTGGCCGTGTTTAAGAACGGACTTTCTATAGGGCTGTTCCCGAAACTACTATT
 498   T  P  H  R  H  K  F  L  P  E  R  Y  P  D  K  G  F  D  D  N   517
      TTATTGCCGCAATCCCGATGGCCAGCCGAGGCCATGGTGCTATACTCTTGACCCTCACAC
1561  ---------+---------+---------+---------+---------+---------+ 1620
      AATAACGGCGTTAGGGCTACCGGTCGGCTCCGGTACCACGATATGAGAACTGGGAGTGTG
 518   Y  C  R  N  P  D  G  Q  P  R  P  W  C  Y  T  L  D  P  H  T   537
      CCGCTGGGAGTACTGTGCAATTAAAACATGCGCTGACAAAGCTGACGACGACGACAAACA
1621  ---------+---------+---------+---------+---------+---------+ 1680
      GGCGACCCTCATGACACGTTAATTTTGTACGCGACTGTTTCGACTGCTGCTGCTGTTTGT
 538   R  W  E  Y  C  A  I  K  T  C  A  D  K  A  D  D  D  D  K  H   557
      CCACCACCACCACCACCACTAGGGTCGAC
1681  ---------+---------+--------- 1709
      GGTGGTGGTGGTGGTGGTGATCCCAGCTG
 558   H  H  H  H  H  H  *           563
```

FIG.2b-3

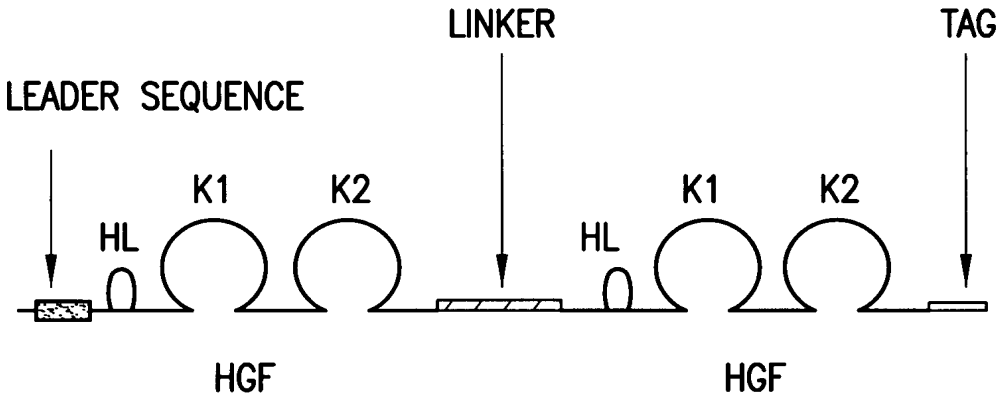

FIG.3a

```
                GGATCCGCCAGCCCGTCCAGCAGCACCATGTGGGTGACCAAACTCCTGCCAGCCCTGCTG
1               ---------+---------+---------+---------+---------+---------+ 60
                CCTAGGCGGTCGGGCAGGTCGTCGTGGTACACCCACTGGTTTGAGGACGGTCGGGACGAC
1                                                M  W  V  T  K  L  L  P  A  L  L  11
                CTGCAGCATGTCCTCCTGCATCTCCTCCTGCTCCCCATCGCCATCCCCTATGCAGAGGGA
61              ---------+---------+---------+---------+---------+---------+ 120
                GACGTCGTACAGGAGGACGTAGAGGAGGACGAGGGGTAGCGGTAGGGGATACGTCTCCCT
12              L  Q  H  V  L  L  H  L  L  L  L  P  I  A  I  P  Y  A  E  G  31
                CAAAGGAAAAGAAGAAATACAATTCATGAATTCAAAAAATCAGCAAAGACTACCCTAATC
121             ---------+---------+---------+---------+---------+---------+ 180
                GTTTCCTTTTCTTCTTTATGTTAAGTACTTAAGTTTTTTAGTCGTTTCTGATGGGATTAG
32              Q  R  K  R  R  N  T  I  H  E  F  K  K  S  A  K  T  T  L  I  51
                AAAATAGATCCAGCACTGAAGATAAAAACCAAAAAAGTGAATACTGCAGACCAATGTGCT
181             ---------+---------+---------+---------+---------+---------+ 240
                TTTTATCTAGGTCGTGACTTCTATTTTTGGTTTTTTCACTTATGACGTCTGGTTACACGA
52              K  I  D  P  A  L  K  I  K  T  K  K  V  N  T  A  D  Q  C  A  71
                AATAGATGTACTAGGAATAAAGGACTTCCATTCACTTGCAAGGCTTTTGTTTTTGATAAA
241             ---------+---------+---------+---------+---------+---------+ 300
                TTATCTACATGATCCTTATTTCCTGAAGGTAAGTGAACGTTCCGAAAACAAAAACTATTT
72              N  R  C  T  R  N  K  G  L  P  F  T  C  K  A  F  V  F  D  K  91
                GCAAGAAAACAATGCCTCTGGTTCCCCTTCAATAGCATGTCAAGTGGAGTGAAAAAAGAA
301             ---------+---------+---------+---------+---------+---------+ 360
                CGTTCTTTTGTTACGGAGACCAAGGGGAAGTTATCGTACAGTTCACCTCACTTTTTTCTT
92              A  R  K  Q  C  L  W  F  P  F  N  S  M  S  S  G  V  K  K  E  111
                TTTGGCCATGAATTTGACCTCTATGAAAACAAAGACTACATTAGAAACTGCATCATTGGT
361             ---------+---------+---------+---------+---------+---------+ 420
                AAACCGGTACTTAAACTGGAGATACTTTTGTTTCTGATGTAATCTTTGACGTAGTAACCA
112             F  G  H  E  F  D  L  Y  E  N  K  D  Y  I  R  N  C  I  I  G  131
                AAAGGACGCAGCTACAAGGGAACAGTATCTATCACTAAGAGTGGCATCAAATGTCAGCCC
421             ---------+---------+---------+---------+---------+---------+ 480
                TTTCCTGCGTCGATGTTCCCTTGTCATAGATAGTGATTCTCACCGTAGTTTACAGTCGGG
132             K  G  R  S  Y  K  G  T  V  S  I  T  K  S  G  I  K  C  Q  P  151
                TGGAGTTCCATGATACCACACGAACACAGCTATCGGGGTAAAGACCTACAGGAAAACTAC
481             ---------+---------+---------+---------+---------+---------+ 540
                ACCTCAAGGTACTATGGTGTGCTTGTGTCGATAGCCCCATTTCTGGATGTCCTTTTGATG
152             W  S  S  M  I  P  H  E  H  S  Y  R  G  K  D  L  Q  E  N  Y  171
```

FIG.3b-1

```
                TGTCGAAATCCTCGAGGGGAAGAAGGGGGACCCTGGTGTTTCACAAGCAATCCAGAGGTA
541             ---------+---------+---------+---------+---------+---------+ 600
                ACAGCTTTAGGAGCTCCCCTTCTTCCCCCTGGGACCACAAAGTGTTCGTTAGGTCTCCAT
172             C  R  N  P  R  G  E  E  G  G  P  W  C  F  T  S  N  P  E  V   191
                CGCTACGAAGTCTGTGACATTCCTCAGTGTTCAGAAGTTGAATGCATGACCTGCAATGGG
601             ---------+---------+---------+---------+---------+---------+ 660
                GCGATGCTTCAGACACTGTAAGGAGTCACAAGTCTTCAACTTACGTACTGGACGTTACCC
192             R  Y  E  V  C  D  I  P  Q  C  S  E  V  E  C  M  T  C  N  G   211
                GAGAGTTATCGAGGTCTCATGGATCATACAGAATCAGGGAAGATTTGTCAGCGCTGGGAT
661             ---------+---------+---------+---------+---------+---------+ 720
                CTCTCAATAGCTCCAGAGTACCTAGTATGTCTTAGTCCGTTCTAAACAGTCGCGACCCTA
212             E  S  Y  R  G  L  M  D  H  T  E  S  G  K  I  C  Q  R  W  D   231
                CATCAGACACCACACCGGCACAAATTCTTGCCTGAAAGATATCCCGACAAGGGCTTTGAT
721             ---------+---------+---------+---------+---------+---------+ 780
                GTAGTCTGTGGTGTGGCCGTGTTTAAGAACGGACTTTCTATAGGGCTGTTCCCGAAACTA
232             H  Q  T  P  H  R  H  K  F  L  P  E  R  Y  P  D  K  G  F  D   251
                GATAATTATTGCCGCAATCCCGATGGCCAGCCGAGGCCATGGTGCTATACTCTTGACCCT
781             ---------+---------+---------+---------+---------+---------+ 840
                CTATTAATAACGGCGTTAGGGCTACCGGTCGGCTCCGGTACCACGATATGAGAACTGGGA
252             D  N  Y  C  R  N  P  D  G  Q  P  R  P  W  C  Y  T  L  D  P   271
                CACACCCGCTGGGAGTACTGTGCAATTAAAACATGCGCTGACAAAGCTTCGGGCGGTGGC
841             ---------+---------+---------+---------+---------+---------+ 900
                GTGTGGGCGACCCTCATGACACGTTAATTTTGTACGCGACTGTTTCGAAGCCCGCCACCG
272             H  T  R  W  E  Y  C  A  I  K  T  C  A  D  K  A  S  G  G  G   291
                GGTTCTGGTGGCGGTGGCTCCGGCGGTGGCGGTTCTCTAGAGGGACAAAGGAAAAGAAGA
901             ---------+---------+---------+---------+---------+---------+ 960
                CCAAGACCACCGCCACCGAGGCCGCCACCGCCAAGAGATCTCCCTGTTTCCTTTTCTTCT
292             G  S  G  G  G  G  S  G  G  G  G  S  L  E  G  Q  R  K  R  R   311
                AATACAATTCATGAATTCAAAAAATCAGCAAAGACTACCCTAATCAAAATAGATCCAGCA
961             ---------+---------+---------+---------+---------+---------+ 1020
                TTATGTTAAGTACTTAAGTTTTTTAGTCGTTTCTGATGGGATTAGTTTTATCTAGGTCGT
312             N  T  I  H  E  F  K  K  S  A  K  T  T  L  I  K  I  D  P  A   331
                CTGAAGATAAAAACCAAAAAAGTGAATACTGCAGACCAATGTGCTAATAGATGTACTAGG
1021            ---------+---------+---------+---------+---------+---------+ 1080
                GACTTCTATTTTTGGTTTTTTCACTTATGACGTCTGGTTACACGATTATCTACATGATCC
332             L  K  I  K  T  K  K  V  N  T  A  D  Q  C  A  N  R  C  T  R   351
                AATAAAGGACTTCCATTCACTTGCAAGGCTTTTGTTTTTGATAAAGCAAGAAAACAATGC
1081            ---------+---------+---------+---------+---------+---------+ 1140
                TTATTTCCTGAAGGTAAGTGAACGTTCCGAAAACAAAAACTATTTCGTTCTTTTGTTACG
352             N  K  G  L  P  F  T  C  K  A  F  V  F  D  K  A  R  K  Q  C   371
                CTCTGGTTCCCCTTCAATAGCATGTCAAGTGGAGTGAAAAAAGAATTTGGCCATGAATTT
1141            ---------+---------+---------+---------+---------+---------+ 1200
                GAGACCAAGGGGAAGTTATCGTACAGTTCACCTCACTTTTTTCTTAAACCGGTACTTAAA
372             L  W  F  P  F  N  S  M  S  S  G  V  K  K  E  F  G  H  E  F   391
```

FIG.3b-2

```
                GACCTCTATGAAAACAAAGACTACATTAGAAACTGCATCATTGGTAAAGGACGCAGCTAC
1201            ---------+---------+---------+---------+---------+---------+ 1260
                CTGGAGATACTTTTGTTTCTGATGTAATCTTTGACGTAGTAACCATTTCCTGCGTCGATG
 392            D  L  Y  E  N  K  D  Y  I  R  N  C  I  I  G  K  G  R  S  Y   411
                AAGGGAACAGTATCTATCACTAAGAGTGGCATCAAATGTCAGCCCTGGAGTTCCATGATA
1261            ---------+---------+---------+---------+---------+---------+ 1320
                TTCCCTTGTCATAGATAGTGATTCTCACCGTAGTTTACAGTCGGGACCTCAAGGTACTAT
 412            K  G  T  V  S  I  T  K  S  G  I  K  C  Q  P  W  S  S  M  I   431
                CCACACGAACACAGCTATCGGGGTAAAGACCTACAGGAAAACTACTGTCGAAATCCTCGA
1321            ---------+---------+---------+---------+---------+---------+ 1380
                GGTGTGCTTGTGTCGATAGCCCCATTTCTGGATGTCCTTTTGATGACAGCTTTAGGAGCT
 432            P  H  E  H  S  Y  R  G  K  D  L  Q  E  N  Y  C  R  N  P  R   451
                GGGGAAGAAGGGGGACCCTGGTGTTTCACAAGCAATCCAGAGGTACGCTACGAAGTCTGT
1381            ---------+---------+---------+---------+---------+---------+ 1440
                CCCCTTCTTCCCCCTGGGACCACAAAGTGTTCGTTAGGTCTCCATGCGATGCTTCAGACA
 452            G  E  E  G  G  P  W  C  F  T  S  N  P  E  V  R  Y  E  V  C   471
                GACATTCCTCAGTGTTCAGAAGTTGAATGCATGACCTGCAATGGGGAGAGTTATCGAGGT
1441            ---------+---------+---------+---------+---------+---------+ 1500
                CTGTAAGGAGTCACAAGTCTTCAACTTACGTACTGGACGTTACCCCTCTCAATAGCTCCA
 472            D  I  P  Q  C  S  E  V  E  C  M  T  C  N  G  E  S  Y  R  G   491
                CTCATGGATCATACAGAATCAGGCAAGATTTGTCAGCGCTGGGATCATCAGACACCACAC
1501            ---------+---------+---------+---------+---------+---------+ 1560
                GAGTACCTAGTATGTCTTAGTCCGTTCTAAACAGTCGCGACCCTAGTAGTCTGTGGTGTG
 492            L  M  D  H  T  E  S  G  K  I  C  Q  R  W  D  H  Q  T  P  H   511
                CGGCACAAATTCTTGCCTGAAAGATATCCCGACAAGGGCTTTGATGATAATTATTGCCGC
1561            ---------+---------+---------+---------+---------+---------+ 1620
                GCCGTGTTTAAGAACGGACTTTCTATAGGGCTGTTCCCGAAACTACTATTAATAACGGCG
 512            R  H  K  F  L  P  E  R  Y  P  D  K  G  F  D  D  N  Y  C  R   531
                AATCCCGATGGCCAGCCGAGGCCATGGTGCTATACTCTTGACCCTCACACCCGCTGGGAG
1621            ---------+---------+---------+---------+---------+---------+ 1680
                TTAGGGCTACCGGTCGGCTCCGGTACCACGATATGAGAACTGGGAGTGTGGGCGACCCTC
 532            N  P  D  G  Q  P  R  P  W  C  Y  T  L  D  P  H  T  R  W  E   551
                TACTGTGCAATTAAAACATGCGCTGACAAAGCTGACGACGACGACAAACACCACCACCAC
1681            ---------+---------+---------+---------+---------+---------+ 1740
                ATGACACGTTAATTTTGTACGCGACTGTTTCGACTGCTGCTGCTGTTTGTGGTGGTGGTG
 552            Y  C  A  I  K  T  C  A  D  K  A  D  D  D  D  K  H  H  H  H   571
                CACCACCACTAGGGTCGAC
1741            ---------+---------  1759
                GTGGTGGTGATCCCAGCTG
 572            H  H  H  *           574
```

FIG.3b-3

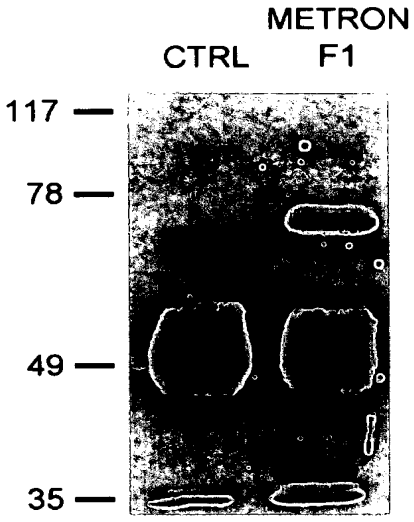

FIG.4

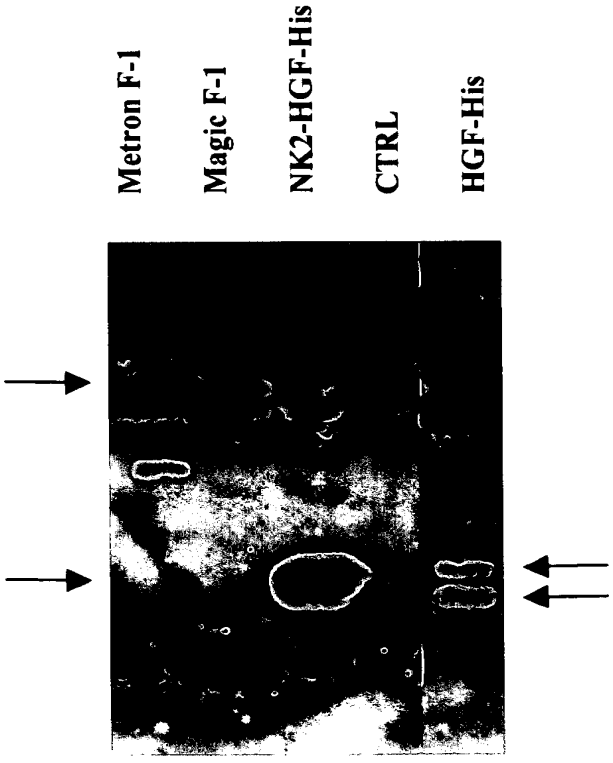

FIG.5a

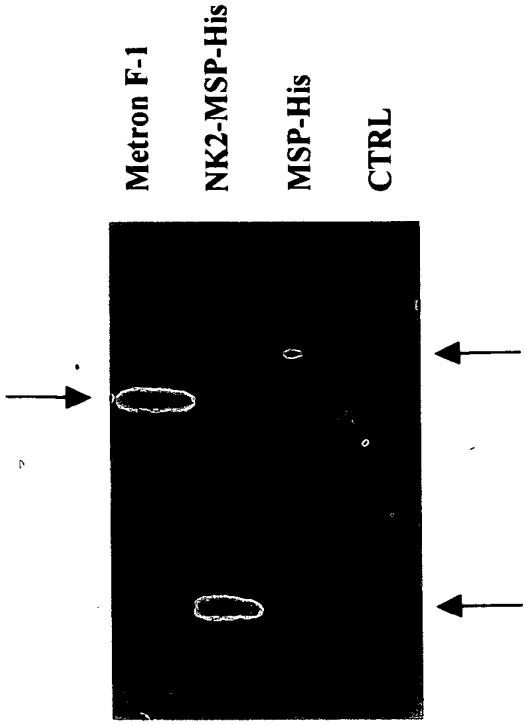

FIG.5b

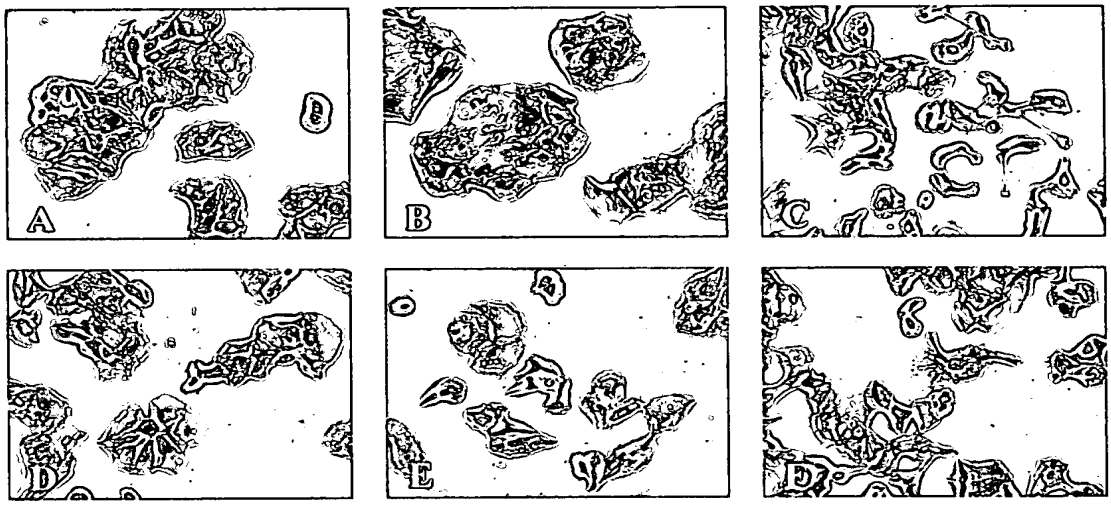

FIG.6

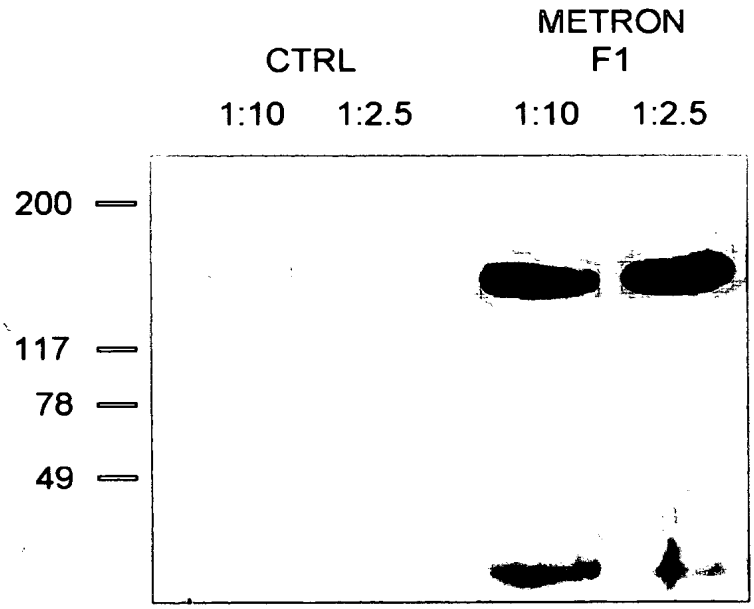

FIG.7

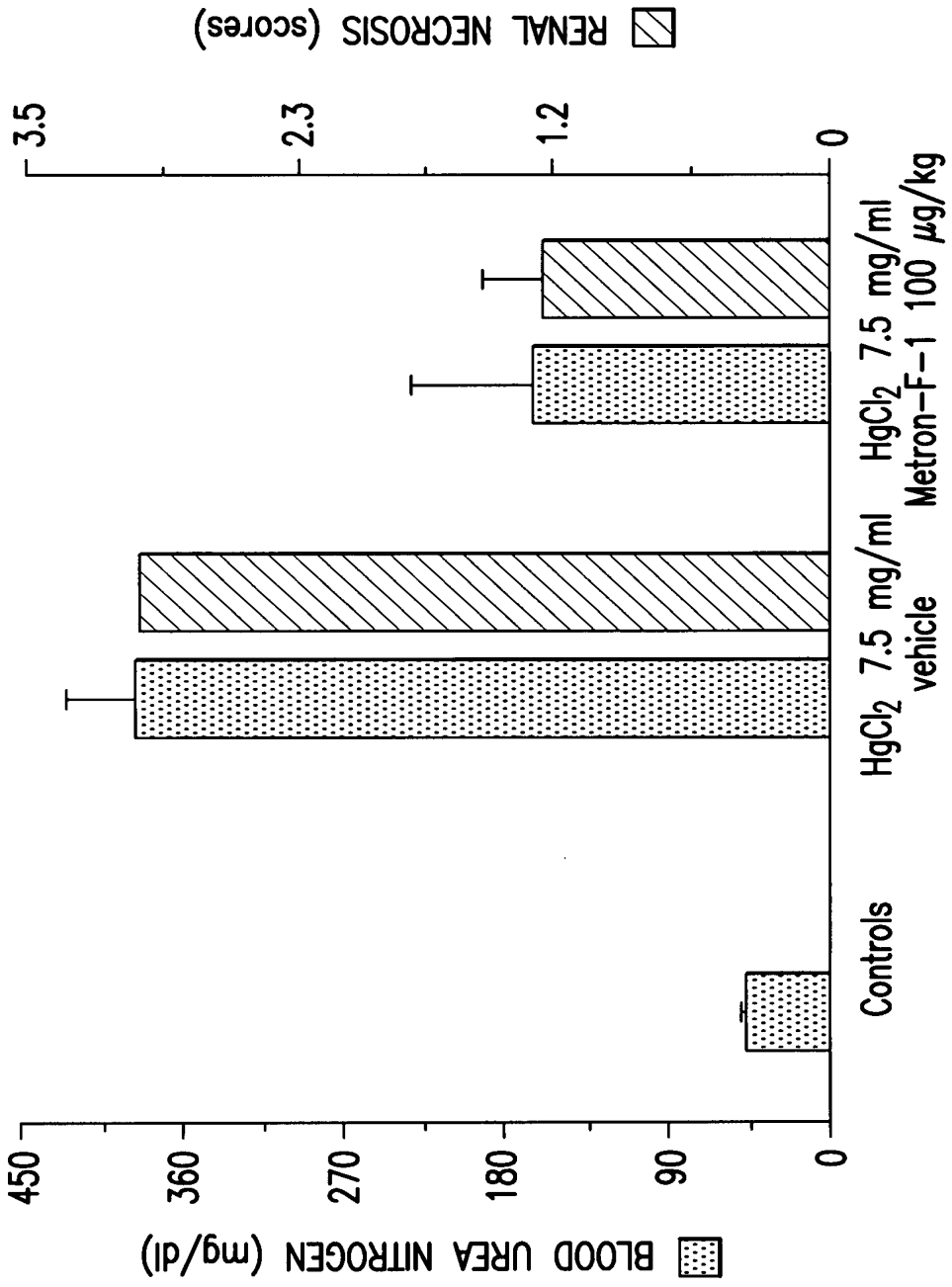

FIG.8